

	9	18	27	36	45	54
5'	C CGC TGC AGC CGC TTT CTG CGG CCT GGG CCT CTC GTG GCC ATG CCA CAC					M P H
	63	72	81	90	99	108
GCC TTC AAG CCC GGG GAC TTG GTG TTC GCT AAG ATG AAG GGC TAC CCT CAC TGG						A F K P G D L V F A K M K G Y P H W
	117	126	135	144	153	162
CCT GCC AGG ATC GAC GAC ATC GCG GAT GGC GCC GTG AAG CCC CCA CCC AAC AAG						P A R I D D I A A D G A V K P P P N K
	171	180	189	198	207	216
TAC CCC ATC TTT TTC TTT GGC ACA CAC GAA ACA GCC TTC CTG GGC CCC AAA GAC						Y P I F F F G T G T H E T A F L G P K D
	225	234	243	252	261	270
CTC TTC CCT TAC GAG GAA TCC AAG GAG AAG TTT GGC AAG CCC AAC AAG AGG AAA						L F P Y E E S K E K F G G K P N K R K
	279	288	297	306	315	324
GGG TTC AGC GAG GGG CTG TGG GAG ATC GAG AAC AAC CCT ACT GTC AAG GCT TCC						G F S E G G L W E I E N N P T V K A S
	333	342	351	360	369	378
GGC TAT CAG TCC TCC CAG AAA AAG AGC TGT GTG GAA GAG CCT GAA CCA GAG CCC						G Y Q S S Q K K S C V E E P E P E P

FIGURE 1A

2015	2014	2013	2012	2011	2010	2009	2008	2007	2006	2005	2004	2003	2002	2001	2000	1999	1998	1997	1996	1995	1994	1993	1992	1991	1990	1989	1988	1987	1986	1985	1984	1983	1982	1981	1980	1979	1978	1977	1976	1975	1974	1973	1972	1971	1970	1969	1968	1967	1966	1965	1964	1963	1962	1961	1960	1959	1958	1957	1956	1955	1954	1953	1952	1951	1950	1949	1948	1947	1946	1945	1944	1943	1942	1941	1940	1939	1938	1937	1936	1935	1934	1933	1932	1931	1930	1929	1928	1927	1926	1925	1924	1923	1922	1921	1920	1919	1918	1917	1916	1915	1914	1913	1912	1911	1910	1909	1908	1907	1906	1905	1904	1903	1902	1901	1900	1899	1898	1897	1896	1895	1894	1893	1892	1891	1890	1889	1888	1887	1886	1885	1884	1883	1882	1881	1880	1879	1878	1877	1876	1875	1874	1873	1872	1871	1870	1869	1868	1867	1866	1865	1864	1863	1862	1861	1860	1859	1858	1857	1856	1855	1854	1853	1852	1851	1850	1849	1848	1847	1846	1845	1844	1843	1842	1841	1840	1839	1838	1837	1836	1835	1834	1833	1832	1831	1830	1829	1828	1827	1826	1825	1824	1823	1822	1821	1820	1819	1818	1817	1816	1815	1814	1813	1812	1811	1810	1809	1808	1807	1806	1805	1804	1803	1802	1801	1800	1799	1798	1797	1796	1795	1794	1793	1792	1791	1790	1789	1788	1787	1786	1785	1784	1783	1782	1781	1780	1779	1778	1777	1776	1775	1774	1773	1772	1771	1770	1769	1768	1767	1766	1765	1764	1763	1762	1761	1760	1759	1758	1757	1756	1755	1754	1753	1752	1751	1750	1749	1748	1747	1746	1745	1744	1743	1742	1741	1740	1739	1738	1737	1736	1735	1734	1733	1732	1731	1730	1729	1728	1727	1726	1725	1724	1723	1722	1721	1720	1719	1718	1717	1716	1715	1714	1713	1712	1711	1710	1709	1708	1707	1706	1705	1704	1703	1702	1701	1700	1699	1698	1697	1696	1695	1694	1693	1692	1691	1690	1689	1688	1687	1686	1685	1684	1683	1682	1681	1680	1679	1678	1677	1676	1675	1674	1673	1672	1671	1670	1669	1668	1667	1666	1665	1664	1663	1662	1661	1660	1659	1658	1657	1656	1655	1654	1653	1652	1651	1650	1649	1648	1647	1646	1645	1644	1643	1642	1641	1640	1639	1638	1637	1636	1635	1634	1633	1632	1631	1630	1629	1628	1627	1626	1625	1624	1623	1622	1621	1620	1619	1618	1617	1616	1615	1614	1613	1612	1611	1610	1609	1608	16
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387	GAA	GCT	GCA	GAG	GGT	GAC	GGT	GAT	AAG	AAG	GGG	AAT	GCA	GAG	GGC	AGC	AGC	GAC	432
	E	A	A	E	G	D	G	D	K	K	G	N	A	E	G	S	S	D	
396																			414
405																			
441	GAG	GAA	GGG	AAG	CTG	GTC	ATT	GAT	GAG	CCA	GCC	AAG	GAG	AAG	AAC	GAG	AAA	GGA	486
	E	E	G	K	L	V	I	D	E	P	A	K	E	K	N	E	K	G	
450																			468
459																			
504	GCG	TTG	AAG	AGG	AGA	GCA	GGG	GAC	TTG	CTG	GAG	GAC	TCT	CCT	AAA	CGT	CCC	AAG	531
	A	L	K	R	R	A	G	D	L	L	E	D	S	P	K	R	P	K	
558																			576
567	GAG	GCA	GAA	AAC	CCT	GAA	GGA	GAG	GAG	AAG	GAG	GCA	GCC	ACC	TTG	GAG	GTT	GAG	585
	E	A	E	N	P	E	G	E	E	K	E	A	A	T	L	E	V	E	
603																			630
612	AGG	CCC	CTT	CCT	ATG	GAG	GTG	GAA	AAG	AAT	AGC	ACC	CCC	TCT	GAG	CCC	GGC	TCT	639
	R	P	L	P	M	E	V	E	K	N	S	T	P	S	E	P	G	S	
666																			684
675	GGC	CGG	GGG	CCT	CCC	CNN	NNN	NNN	NNN	NNN	NNN	NNN	NNN	NNN	NAG	GAA	GAG	GCT	693
	G	R	G	P	P	X	X	X	X	X	X	X	X	X	X	E	E	A	
711																			738
720	ACC	AAG	GAA	GAT	GCT	GAG	GCC	CCA	GGC	ATC	AAG	AGT	CAT	GAG	AGC	CTG	TAG	CCA	747
	T	K	E	D	A	E	A	P	G	I	K	S	H	E	S	L			

FIGURE 1B

Figure 1C

765	774	783	792	801	810
CCA ATG TTT CAA GAG GAG CCC CCA CCC TGT TCC TGC TGC TGT CTG GGT GCT ACT					
819	828	837	846	855	864
GGG GAA ACT GGC CAT GGG CTG CAA ACT GGG NAC CCC TTT TCC ANC NCA ANC TGN					

TNT TCT T 3'

FIGURE 1C

1 M P H A - - - - F K P G D L V F A K M K G Y P H W P A R I D D I A D G A V K P 876242
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 598956
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 945419

36 P P N K Y P I F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K 876242
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K GI 598956
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K GI 945419

76 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E P E A A E 876242
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E P E A A E GI 598956
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C A A E P E V E P E A H E GI 945419

116 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D 876242
121 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D GI 598956
121 G D G D K K G S A E G S S D E E G K L V I D E P A K E K N E K G T L K R R A G D GI 945419

156 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T 876242
161 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T GI 598956
161 V L E D S P K R P K E S G D H E E D K E I A A L E G E R H L P V E V E K N S T GI 945419

196 P S E P G S G R G P P X X X X X X X X X E E A T K E D A E A P G I K S H E S L 876242
201 P S E P G S G R G P P Q E E E E E E D E E E E A T K E D A E A P G I R D H E S L GI 598956
201 P S E P D S G Q G P P A E E E E E G E - - - E E A A K E E A E A P G V R D H E S L GI 945419

FIGURE 2

Figure 3A: Sequence

1 CCGCTGCAAGCCGCTTTCTGCGGCCCTGGGCCCTCTCGCCGTC n876242
 1 ATGTCGA-----TCAACCGGC g598956
 41 AGCATGCCACACGCCCTTCAAGCCCGGGGACCTTGGGTGTTCTG n876242
 20 AGAAGGA-GTAC-----AAATGCGGGGACCTGGGTGTTCTG g598956
 81 CTAAAGATGAAGGGCTACCCCTCACTGGCCCTGCCAGGATCTGA n876242
 53 CAAAGATGAAGGGCTACCCCAACTGGCCGGCCCGGATTGA g598956
 121 CGACATCGCGGATGGCGCGCGTGAAAGCCCCCAACCAAG n876242
 93 CGAATGCCTGAGCTGGCGCGTGAATCAACAGCCCAACAA g598956
 161 TACCCCATCTTTTCTTTTGGCAACACGAACAAGCCTTCTC n876242
 133 TACCAAGTCTTTTTTTGGGACCCACGAAGACGCTTCTC g598956
 201 TGGGCCCAAGACCTCTTCCCTTACGAGGAATCCAAGGA n876242
 173 TGGGCCCAAGACCTCTTCCCTTACGAGGAATCCAAGGA g598956
 241 GAAAGTTTGGCAAGCCCAACAAGAGGAAGGTTTCAAGCGAG n876242
 213 GAAAGTTTGGCAAGCCCAACAAGAGGAAGGTTTCAAGCGAG g598956
 281 GGGCTGTGGAGATCGAGAAACAACCTACTGTCAAGGCTT n876242
 253 GGGCTGTGGAGATCGAGAAACAACCTACTGTCAAGGCTT g598956
 321 CCGGCTATCAGTCCCTCCAGAAACAAGAGCTGTGGAAGA n876242
 293 CCGGCTATCAGTCCCTCCAGAAACAAGAGCTGTGGAAGA g598956

FIGURE 3A

Figure 3B

361 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G T G A C G G T G A T n876242
 333 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G T G A C G G T G A T g598956

 401 A A G A A G G G G A A T G C A G A G G G C A G C A G C G A C G A G G A A G G G A n876242
 373 A A G A A G G G G A A T G C A G A G G G C A G C A G C G A C G A G G A A G G G A g598956

 441 A G C T G G T C A T T G A T G A G C C C A G C C A A G G A G A A C G A G A A n876242
 413 A G C T G G T C A T T G A T G A G C C C A G C C A A G G A G A A C G A G A A g598956

 481 A G G A G C C G T T G A A G A G G A G A G C A G G G A C T T G C T G G A G G A C n876242
 453 A G G A G C C G T T G A A G A G G A G A G C A G G G A C T T G C T G G A G G A C g598956

 521 T C T C C T A A A C G T C C C A A G G A G G C A G A A A C C C T G A A G G A G n876242
 493 T C T C C T A A A C G T C C C A A G G A G G C A G A A A C C C T G A A G G A G g598956

 561 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G C C C C T n876242
 533 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G C C C C T g598956

 601 T C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C n876242
 573 T C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C g598956

 641 G G C T C T G G C C G G G G G C C T C C C C N N N N N N N N N N N N N n876242
 613 G G C T C T G G C C G G G G G C C T C C C C A A G A G G A A G A A G A G A G G g598956

FIGURE 3B

Figure 3C

681	NNNNNNNN	AGGAAGAGGCTACCAAGGAAGATGCTGAGGC	n876242
653	<u>AGGATGAAG</u>	AGGAAGAGGCTACCAAGGAAGATGCTGAGGC	g598956
721	CCAGGCATCAAGAGTCA	TGAGAGCCCTGTAGCCACCAATG	n876242
693	CCAGGCATCA	<u>GAGA</u> TCA	TGAGAGCCCTGTAG
761	TTTCAAGAGGAGCCCC	CACTGTTCTGCTGCTGCTG	n876242
723			g598956
801	GTGCTACTGGGGGAA	AACTGGGCCCTGC	AACTGGGNA
723			n876242
841	CCCCTTT	TCCANCNC	ACTGNTTCTT
723			g598956

FIGURE 3C

04280" 9886660

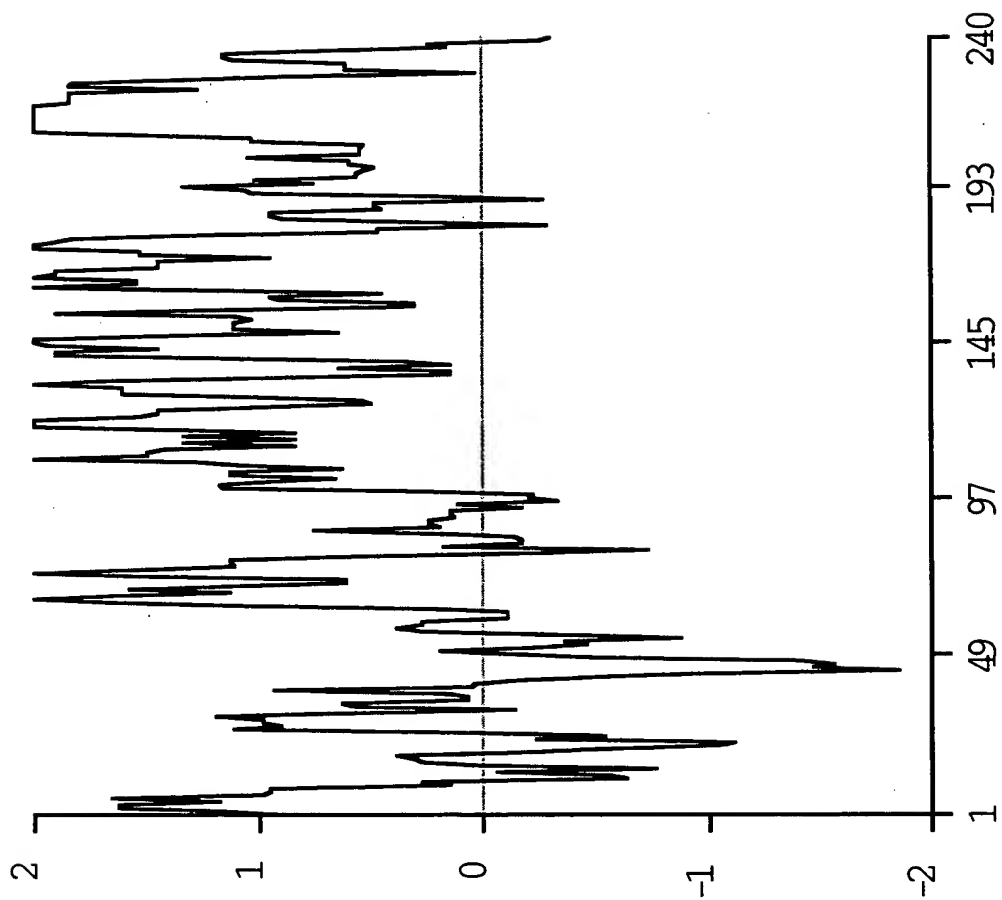


FIGURE 4B

Library	Lib Description	Abun	Pct Abun
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	5	0.3425
THP1PLB02	THP-1 promonocyte cell line, treated PMA, LPS	4	0.1630
THP1PEB01	THP-1 promonocyte cell line, treated PMA	3	0.1463
PANCDIT03	pancreas, NIDDM, 57 M	1	0.1462
THP1T7T01	THP1 cells, untreated	3	0.1447
BSTMNOT01	brain stem, 72 M	1	0.1214
PROSTUT12	prostate tumor, 65 M, match to PROSNOT20	4	0.1118
HUVESTB01	HUVEC endothelial cell line, shear stress	3	0.1078
PENITUT01	penis tumor, carcinoma, 64 M	4	0.1066
AMLBNOT01	AML blast cells, blast crisis, 58 F	1	0.1058
COLNNOT13	colon, ascending, 28 M	3	0.0932
HUVENOB01	HUVEC endothelial cell line, control	2	0.0841
UTRSNOT05	uterus, 45 F	3	0.0834
SINTNOT13	small intestine, ileum, ulcerative cholangitis, 25 F	3	0.0826
LUNGNOT03	lung tumor, 69 M, match to LUNGNOT15	5	0.0796
OVARNOT01	ovary, 49 F, WM	1	0.0752
PLACNOT02	placenta, neonatal F, NORM, WM	13	0.0722
PROSNOT01	prostate, 78 M	2	0.0702
SPLNFEM01	spleen, fetal, WM	2	0.0663
COLNNOT19	large intestine, cecum, 18 F	2	0.0585
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	4	0.0580
COLNFET02	colon, fetal F	4	0.0571

FIGURE 5A

THP1NOT01	THP1 cells, untreated	1	0.0571
LUNGNOT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	3	0.0567
SININOT01	small intestine, ileum, 4 F	2	0.0560
THP1AZT01	THP-1 promonocyte cell line, treated AZ	1	0.0554
LUNGNOT15	lung, 69 M, match to LUNGNOT03	2	0.0553
LIVRFET02	liver, fetal F	2	0.0550
KERANOT02	keratinocytes, primary cell line, 30 F	3	0.0546
PROSTUT09	prostate tumor, 66 M	2	0.0529
LEUKNOT03	white blood cells, 27 F	2	0.0523
TESTNOT03	testis, 37 M	4	0.0515
COLNPOT01	colon polyp, 40 F	2	0.0513
PROSNOT14	prostate, 60 M, match to PROSTUT08	2	0.0512
BRAITUT02	brain tumor, metastasis, 58 M	3	0.0509
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	5	0.0493
TESTNOT01	testis, 37 M	1	0.0478
UCMCNOT02	mononuclear cells	2	0.0471
THP1PLB01	THP-1 promonocyte cell line, treated PMA, LPS	1	0.0452
BRSTNOT02	breast, 55 F, match to BRSTTUT01	4	0.0443
PROSNOT02	prostate, 50 M, match to PROSTUT01	1	0.0435
COLNNOT08	colon, 60 M	1	0.0426
PANCTUT02	pancreatic tumor, carcinoma, 45 F	2	0.0403
SCORNOT01	spinal cord, 71 M	2	0.0402
UTRSNOT01	uterus, 59 F	1	0.0394
SINTTUT01	small intestine tumor, ileum, 42 M	1	0.0382

FIGURE 5B

TYMNOT01	lymphocytes (non-adher PBMNC), 24 M, RP	1	0.0379
HNT2RAT01	hNT2 cell line, teratocarcinoma, treated RA	2	0.0376
BRAINOT03	brain, 26 M	2	0.0371
LUNGNOT04	lung, 2 M	2	0.0366
PROSNOT20	prostate, 65 M, match to PROSTUT12	1	0.0336
CARDFEM01	heart, fetal, NORM, WM	3	0.0335
OVARTUT01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0323
OVARNOT02	ovary, 59 F	1	0.0316
NEUTGMT01	granulocytes, periph blood, M/F, treated GM-CSF	2	0.0313
BRSTNOT05	breast, 58 F, match to BRSTTUT03	2	0.0309
STOMNOT02	stomach, 52 M, match to STOMTUT01	1	0.0308
BRSTNOT07	breast, 43 F	1	0.0307
STOMNOT01	stomach, 55 M	1	0.0303
LUNGNOT18	lung, 66 F	1	0.0298
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
COLNTUT06	large intestine, cecal tumor, 45 F	1	0.0293
LIVSFEM02	liver/spleen, fetal M, NORM, WM	11	0.0290
BEPINOT01	bronchial epithelium, primary cell line, 54 M	2	0.0289
PANCNOT07	pancreas, fetal M	1	0.0287
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
LUNGNOT12	lung, 78 M	1	0.0278
TESTTUT02	testicular tumor, 31 M	1	0.0278

FIGURE 5C

THYRTUT03	thyroid tumor, benign, 17 M	1	0.0276
LATRTUT02	heart tumor, myoma, 43 M	2	0.0275
BEPINON01	bronchial epithelium, 1° cell line, 54 M, NORM	1	0.0274
OVARNOT07	ovary, 28 F	1	0.0269
PTHYTUM01	parathyroid tumor, adenoma, M/F, NORM, WM	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
LATRNOT01	heart, left atrium, 51 F	1	0.0266
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266
BRSTNOM01	breast, F, NORM, WM	1	0.0264
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262
DUODNOT02	small intestine, duodenum, 8 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
BRAITUT07	brain tumor, left frontal, 32 M	1	0.0259
LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259
PROSNOT18	prostate, 58 M	1	0.0256
PANCNOT08	pancreas, 65 F, match to PANCTUT01	1	0.0254
BLADTUT04	bladder tumor, 60 M, match to BLADNOT05	2	0.0253
PLACNOB01	placenta, neonatal F	1	0.0251
LUNGNOT02	lung, 47 M	1	0.0246
TMLR3DT02	lymphocytes (non-adher PBMC), M/F, 72-hr MLR	1	0.0246
HIPONOT01	brain, hippocampus, 72 F	1	0.0239
RATRNOT02	heart, right atrium, 39 M	1	0.0237
MMLR1DT01	macrophages (adher PBMC), M/F, 24-hr MLR	1	0.0236

FIGURE 5D

TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	1	0.0229
PROSNOT06	prostate, 57 M, match to PROSTUT04	2	0.0228
LIVRNOT01	liver, 49 M	1	0.0198
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0196
CRBLNOT01	brain, cerebellum, 69 M	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0194
BRSTNOT04	breast, 62 F	2	0.0192
MELANOM01	melanocytes, M, NORM, WM	2	0.0192
LUNGAST01	lung, asthma, 17 M	2	0.0189
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMNC), M/F, 48-hr MLR	1	0.0178
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174
HNT2NOT01	hNT2 cell line, teratocarcinoma, control	1	0.0173
UCMCL5T01	mononuclear cells, treated IL-5	2	0.0168
CONNNOT01	fat, mesentary, 71 M	1	0.0149
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	1	0.0134
SINTFET03	small intestine, fetal F	1	0.0130
KIDNNOT05	kidney, neonatal F	1	0.0106
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0103
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0095
LUNGFET03	lung, fetal F	1	0.0091
BRAINOM01	brain, infant F, NORM, WM	1	0.0045

FIGURE 5E